



COMPARISON A: SEQ ID NO. 1 (top line) vs. SEQ ID NO. 2 (bottom line) (17 pages)

1	GAAGAGTTGATTGAGAAGTGCCTCTTGGTTAAGGATTAACCACAGGGAAAAATCCAGCAG	60	66
1	GAAGAGTTGATTGAGAAGTGCCTCTTGGTTAAGGATTAACCACAGGGAAAAATCCAGCAG	60	66
61	AAACAGAAGAACTGTGGGTTTCTTACCCCAGCCCTCAAGGAAGCTATGCCGTGAAAGGGG	120	126
61	AAACAGAAGAACTGTGGGTTTCTTACCCCAGCCCTCAAGGAAGCTATGCCGTGAAAGGGG	120	126
121	TACTGATACACTGACATACAGCAAGTTGGACGGGGCATCAGTTCTTCATTTGTGGAGTGG	180	186
121	TACTGATACACTGACATACAGCAAGTTGGACGGGGCATCAGTTCTTCATTTGTGGAGTGG	180	186
181	AGAAAAGAAGAGGAAATCTCTCATTGGGGCATTGAAGGATGGCTTCCCTGTTTCATCA	240	246
181	AGAAAAGAAGAGGAAATCTCTCATTGGGGCATTGAAGGATGGCTTCCCTGTTTCATCA	240	246
241	GCTTCAGATCCTGGTCTGGAAAAATTGGCTAGGTGTAAAAAGGCAGCCGCTTTGGACACT	300	306
241	GCTTCAGATCCTGGTCTGGAAAAATTGGCTAGGTGTAAAAAGGCAGCCGCTTTGGACACT	300	306
301	TGTCTTGATCTTATGGCCAGTCATTATTTTCATAATTTTGGCTATTACTCGGACCAAATT	360	366
301	TGTCTTGATCTTATGGCCAGTCATTATTTTCATAATTTTGGCTATTACTCGGACCAAATT	360	366
361	TCCTCCAAGTCAAAACCAACTTGTTACCTCGCACCTCGAAACCTTCCTAGTACTGGATT	420	426
361	TCCTCCAAGTCAAAACCAACTTGTTACCTCGCACCTCGAAACCTTCCTAGTACTGGATT	420	426
421	CTTTCCATTTCCTGCAGACCCTACTCTGTGACACAGACTCTAAATGCAAAGACACACCCTA	480	486
421	CTTTCCATTTCCTGCAGACCCTACTCTGTGACACAGACTCTAAATGCAAAGACACACCCTA	480	486
481	TGGCCCACAAGATCTGCTTCGTAGGAAAGGAATTGATGATGCACTATTTAAAGACAGTGA	540	546
481	TGGCCCACAAGATCTGCTTCGTAGGAAAGGAATTGATGATGCACTATTTAAAGACAGTGA	540	546

COMPARISON A: SEO ID NO. 1 (top line) vs. SEQ ID NO. 2 (bottom line) (17 pages)

[illegible]

COMPARISON A: SEQ ID NO. 1 (top line) vs. SEQ ID NO. 2 (bottom line) (17 pages)

1081	AAAGGCAAACAGTGTGCTGCTGGTTGTGCAGAAGGTTTATCCACGTTTTGCAACTAACGA	1140	1146
1081	AAAGGCAAACAGTGTGCTGCTGGTTGTGCAGAAGGTTTATCCACGTTTTGCAACTAACGA	1140	1146
1141	AGGTTTCAGAACCCTCCAGAAGTCTGTAAACATCTGCTGTACACTCTGGACTCCCCAGC	1200	1206
1141	AGGTTTCAGAACCCTCCAGAAGTCTGTAAACATCTGCTGTACACTCTGGACTCCCCAGC	1200	1206
1201	TCAAGGTGACTCCGATAATATAACGCATGTGTGGAATGAGGATGATGGACAGACCTTATC	1260	1266
1201	TCAAGGTGACTCCGATAATATAACGCATGTGTGGAATGAGGATGATGGACAGACCTTATC	1260	1266
1261	TCCAAGCAGTCTGGCTGCACAGCTCCTAATTCTGGAAAACCTTGAAGATGCCCTCTTAAA	1320	1326
1261	TCCAAGCAGTCTGGCTGCACAGCTCCTAATTCTGGAAAACCTTGAAGATGCCCTCTTAAA	1320	1326
1321	TATATCAGCAAATAGTCTTATATTCCTTACTTGGCATGTGTGAGAAATGTGACTGACAG	1380	1386
1321	TATATCAGCAAATAGTCTTATATTCCTTACTTGGCATGTGTGAGAAATGTGACTGACAG	1380	1386
1381	TTTGGCCAGAGGTTTACCAGAAAATCTAAGACTCCTGCAGTCCACAATACGATTTAAAAA	1440	1446
1381	TTTGGCCAGAGGTTTACCAGAAAATCTAAGACTCCTGCAGTCCACAATACGATTTAAAAA	1440	1446
1441	ATCTTTTCTTCGCAATGGTTCCTATGAAGATTACTTTCTCCAGTTCCTGAAGTCCTAAA	1500	1506
1441	ATCTTTTCTTCGCAATGGTTCCTATGAAGATTACTTTCTCCAGTTCCTGAAGTCCTAAA	1500	1506
1501	ATCAAACTGTCTCAACTTCGAAACTTGACCGAACTTCTTTGTGAATCTGAAACTTTCAG	1560	1566
1501	ATCAAACTGTCTCAACTTCGAAACTTGACCGAACTTCTTTGTGAATCTGAAACTTTCAG	1560	1566
1561	TTTGATAGAGAAGTCATGCCAGCTCTCTGATATGAGCTTTGGGAGCCTGTGTGAAGAAAG	1620	1626
1561	TTTGATAGAGAAGTCATGCCAGCTCTCTGATATGAGCTTTGGGAGCCTGTGTGAAGAAAG	1620	1626

COMPARISON A: SEQ ID NO. 1 (top line) vs. SEQ ID NO. 2 (bottom line) (17 pages)

1621	TGAGTTTGATCTGCAACTCCTCGAAGCGGCAGAGCTGGGCACCGAAATAGCAGCCAGCTT	1680	1686
1621			
1621	TGAGTTTGATCTGCAACTCCTCGAAGCGGCAGAGCTGGGCACCGAAATAGCAGCCAGCTT	1680	1686
	o o o o o o		
1681	ACTGTACCATGACAATGTCATATCTAAAAAAGTGAGAGATTTGCTGACTGGAGATCCAAG	1740	1746
1681			
1681	ACTGTACCATGACAATGTCATATCTAAAAAAGTGAGAGATTTGCTGACTGGAGATCCAAG	1740	1746
	o o o o o o		
1741	CAAATTAATTTAAATATGGATCAGTTTCTAGAACAGGCACTGCAAATGAATTACTTGGA	1800	1806
1741			
1741	CAAATTAATTTAAATATGGATCAGTTTCTAGAACAGGCACTGCAAATGAATTACTTGGA	1800	1806
	o o o o o o		
1801	AAATATCACTCAGTTAATACCGATCATAGAAGCCATGCTGCATGTCAATAACAGTGCAGA	1860	1866
1801			
1801	AAATATCACTCAGTTAATACCGATCATAGAAGCCATGCTGCATGTCAATAACAGTGCAGA	1860	1866
	o o o o o o		
1861	TGCTTCTGAAAAGCCAGGTCAGTTACTAGAAATGTTTAAAAATGTTGAAGAGCTGAAAGA	1920	1926
1861			
1861	TGCTTCTGAAAAGCCAGGTCAGTTACTAGAAATGTTTAAAAATGTTGAAGAGCTGAAAGA	1920	1926
	o o o o o o		
1921	AGATTTAAGGAGAACAACAGGAATGTCCAACAGGACTATTGACAAGTTGCTGGCCATTCC	1980	1986
1921			
1921	AGATTTAAGGAGAACAACAGGAATGTCCAACAGGACTATTGACAAGTTGCTGGCCATTCC	1980	1986
	o o o o o o		
1981	CATCCCTGATAATAGAGCTGAGATTATTTCTCAGGTGTTCTGGCTGCATTCCTGTGATAC	2040	2046
1981			
1981	CATCCCTGATAATAGAGCTGAGATTATTTCTCAGGTGTTCTGGCTGCATTCCTGTGATAC	2040	2046
	o o o o o o		
2041	TAATATCACTACTCCCAAAGTAGAAGATGCAATGAAAGAATTCTGCAACCTGTCTCTTTC	2100	2106
2041			
2041	TAATATCACTACTCCCAAAGTAGAAGATGCAATGAAAGAATTCTGCAACCTGTCTCTTTC	2100	2106
	o o o o o o		
2101	AGAGAGATCCCGGCAGTCTTACCTCATCGGACTCACCTTCTGCACTACTTAAACATTTA	2160	2166
2101			
2101	AGAGAGATCCCGGCAGTCTTACCTCATCGGACTCACCTTCTGCACTACTTAAACATTTA	2160	2166
	o o o o o o		

COMPARISON A: SEQ ID NO. 1 (top line) vs. SEQ ID NO. 2 (bottom line) (17 pages)

2161	CAACTTCACAGACAAGGTGTTTTTCCCGAGGAAAGATCAAAAGCCAGTAGAAAAGATGAT	2220	2226
2161	CAACTTCACAGACAAGGTGTTTTTCCCGAGGAAAGATCAAAAGCCAGTAGAAAAGATGAT	2220	2226
2221	GGAGCTCTTCATAAGACTAAAAGAGATTCTCAATCAGATGGCTTCTGGCACACATCCGCT	2280	2286
2221	GGAGCTCTTCATAAGACTAAAAGAGATTCTCAATCAGATGGCTTCTGGCACACATCCGCT	2280	2286
2281	GCTAGACAAAATGAGATCCCTGAAGCAAATGCATCTGCCCAGAAGTGTTCCATTAACACA	2340	2346
2281	GCTAGACAAAATGAGATCCCTGAAGCAAATGCATCTGCCCAGAAGTGTTCCATTAACACA	2340	2346
2341	GGCAATGTACAGAAGCAACCGAATGAACACACCACAAGGATCATTTAGCACCATCTCCCA	2400	2406
2341	GGCAATGTACAGAAGCAACCGAATGAACACACCACAAGGATCATTTAGCACCATCTCCCA	2400	2406
2401	AGCATTATGTTCTCAAGGAATTACCACTGAATATTTAACTGCCATGCTGCCCTCTTCCCA	2460	2466
2401	AGCATTATGTTCTCAAGGAATTACCACTGAATATTTAACTGCCATGCTGCCCTCTTCCCA	2460	2466
2461	GAGGCCAAAAGGCAACCAACCAAGGATTTTTTGAAGTTATAAATTAAGAGCAAAAT	2520	2526
2461	GAGGCCAAAAGGCAACCAACCAAGGATTTTTTGAAGTTATAAATTAAGAGCAAAAT	2520	2526
2521	TGCTTCAAAATATGGAATTCCCATAAATACCACACCATTTTGCTTCTCCCTTTATAAAGA	2580	2586
2521	TGCTTCAAAATATGGAATTCCCATAAATACCACACCATTTTGCTTCTCCCTTTATAAAGA	2580	2586
2581	CATCATTAACATGCCCGCTGGACCTGTGATTTGGGCTTCTTGAAACCTATGTTGTTGGG	2640	2646
2581	CATCATTAACATGCCCGCTGGACCTGTGATTTGGGCTTCTTGAAACCTATGTTGTTGGG	2640	2646
2641	AAGAATTTTGCATGCACCATATAACCCAGTCACAAAGGCAATAATGGAAAAGTCCAATGT	2700	2706
2641	AAGAATTTTGCATGCACCATATAACCCAGTCACAAAGGCAATAATGGAAAAGTCCAATGT	2700	2706

COMPARISON A: SEQ ID NO. 1 (top line) vs. SEQ ID NO. 2 (bottom line) (17 pages)

2701	AACTCTGAGACAGCTGGCGGAATTAAGAGAAAAATCTCAAGAGTGGATGGATAAGTCGCC	2760	2766
2701			
2701	AACTCTGAGACAGCTGGCGGAATTAAGAGAAAAATCTCAAGAGTGGATGGATAAGTCGCC	2760	2766
	o o o o o o		
2761	ACTTTTCATGAATTCCTTCCATCTGTTAAACCAGGCAATTCCAATGCTCCAGAATACTCT	2820	2826
2761			
2761	ACTTTTCATGAATTCCTTCCATCTGTTAAACCAGGCAATTCCAATGCTCCAGAATACTCT	2820	2826
	o o o o o o		
2821	AAGGAACCCTTTTGTGCAAGTTTTTGTAAAGTTCTCCGTGGGACTCGATGCTGTTGAACT	2880	2886
2821			
2821	AAGGAACCCTTTTGTGCAAGTTTTTGTAAAGTTCTCCGTGGGACTCGATGCTGTTGAACT	2880	2886
	o o o o o o		
2881	ATTGAAACAGATAGATGAACTCGATATTCTAAGACTGAAATTAGAGAACAACATTGACAT	2940	2946
2881			
2881	ATTGAAACAGATAGATGAACTCGATATTCTAAGACTGAAATTAGAGAACAACATTGACAT	2940	2946
	o o o o o o		
2941	CATCGATCAGCTTAACACACTATCTTCCCTGACAGTAAATATTTCTCTTGTGTATTATA	3000	3006
2941			
2941	CATCGATCAGCTTAACACACTATCTTCCCTGACAGTAAATATTTCTCTTGTGTATTATA	3000	3006
	o o o o o o		
3001	TGACCGTATTCAGGCAGCAAAAACCATAGATGAAATGGAGAGAGAGGCTAAAAGGCTCTA	3060	3066
3001			
3001	TGACCGTATTCAGGCAGCAAAAACCATAGATGAAATGGAGAGAGAGGCTAAAAGGCTCTA	3060	3066
	o o o o o o		
3061	CAAAAGCAACGAACTCTTTGGAAGTGTTATTTTAAAGCTTCCTTCTAACAGAAGCTGGCA	3120	3126
3061			
3061	CAAAAGCAACGAACTCTTTGGAAGTGTTATTTTAAAGCTTCCTTCTAACAGAAGCTGGCA	3120	3126
	o o o o o o		
3121	CAGAGGCTATGACTCTGGAAATGTCTTTCTTCCTCCTGTCATAAAATATACCATCCGGAT	3180	3186
3121			
3121	CAGAGGCTATGACTCTGGAAATGTCTTTCTTCCTCCTGTCATAAAATATACCATCCGGAT	3180	3186
	o o o o o o		
3181	GAGTCTCAAGACCGCACAGACCACAAGAAGCCTAAGAACCAAGATTTGGGCTCCAGGGCC	3240	3246
3181			
3181	GAGTCTCAAGACCGCACAGACCACAAGAAGCCTAAGAACCAAGATTTGGGCTCCAGGGCC	3240	3246
	o o o o o o		

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COMPARISON A: SEQ ID NO. 1 (top line) vs. SEQ ID NO. 2 (bottom line) (17 pages)

3781	CTTTCATTATTTATTGTTCTGGTTACAGTGGAGAATGAGTTGAGCTATGTATTGAAAGTGTT	3840	3846
3781	CTTTCATTATTTATTGTTCTGGTTACAGTGGAGAATGAGTTGAGCTATGTATTGAAAGTGTT	3840	3846
	o		
3841	CATGAGCCTGCTGTCCCCAACAGCATTTCAGCTATGCAAGCCAATACATTGCACGATACGA	3900	3906
3841	CATGAGCCTGCTGTCCCCAACAGCATTTCAGCTATGCAAGCCAATACATTGCACGATACGA	3900	3906
	o		
3901	AGAACAGGGCATTGGTCTTCAGTGGGAAAATATGTACACCTCCCCGGTTCAGGATGACAC	3960	3966
3901	AGAACAGGGCATTGGTCTTCAGTGGGAAAATATGTACACCTCCCCGGTTCAGGATGACAC	3960	3966
	o		
3961	CACCTCATTTGGCTGGCTGTGCTGTCTAATCCTAGCTGACTCTTTCATTTATTTTCCTTAT	4020	4026
3961	CACCTCATTTGGCTGGCTGTGCTGTCTAATCCTAGCTGACTCTTTCATTTATTTTCCTTAT	4020	4026
	o		
4021	TGCTTGGTATGTCAGGAATGTCTTCCCAGGGACATACGGTATGGCAGCTCCCTGGTATTT	4080	4086
4021	TGCTTGGTATGTCAGGAATGTCTTCCCAGGGACATACGGTATGGCAGCTCCCTGGTATTT	4080	4086
	o		
4081	TCCAATTCTTCCTTCCTATTGGAAGGAGCGATTTGGGTGTGCAGAGGTGAAGCCTGAGAA	4140	4146
4081	TCCAATTCTTCCTTCCTATTGGAAGGAGCGATTTGGGTGTGCAGAGGTGAAGCCTGAGAA	4140	4146
	o		
4141	GAGCAATGGCCTCATGTTTACTAACATCATGATGCAGAACACCAACCCATCTGCCAGTCC	4200	4206
4141	GAGCAATGGCCTCATGTTTACTAACATCATGATGCAGAACACCAACCCATCTGCCAGTCC	4200	4206
	o		
4201	TGAATACATGTTTTCTCTAACATCGAGCCTGAACCTAAAGATCTCACAGTCGGGGTTGC	4260	4266
4201	TGAATACATGTTTTCTCTAACATCGAGCCTGAACCTAAAGATCTCACAGTCGGGGTTGC	4260	4266
	o		
4261	CCTGCATGGGGTCACAAAGATCTATGGCTCAAAGTTGCTGTTGATAACCTCAATCTGAA	4320	4326
4261	CCTGCATGGGGTCACAAAGATCTATGGCTCAAAGTTGCTGTTGATAACCTCAATCTGAA	4320	4326
	o		

COMPARISON A: SEQ ID NO. 1 (top line) vs. SEQ ID NO. 2 (bottom line) (17 pages)

4321	CTTTTATGAAGGGCATATTACTTCATTGCTGGGGCCCAATGGAGCTGGGAAAAC TACTAC	4380	4386
4321			
4321	CTTTTATGAAGGGCATATTACTTCATTGCTGGGGCCCAATGGAGCTGGGAAAAC TACTAC	4380	4386
	o o o o o o		
4381	CATTTCCATGT TAACTGGGCTGTTTGGGGCCTCAGCAGGCACCATTTTGTATATGGAAA	4440	4446
4381			
4381	CATTTCCATGT TAACTGGGCTGTTTGGGGCCTCAGCAGGCACCATTTTGTATATGGAAA	4440	4446
	o o o o o o		
4441	AGATATCAAAACAGACCTACACACGGTACGGAAGAACATGGGAGTCTGTATGCAGCACGA	4500	4506
4441			
4441	AGATATCAAAACAGACCTACACACGGTACGGAAGAACATGGGAGTCTGTATGCAGCACGA	4500	4506
	o o o o o o		
4501	CGTCTTGTT CAGTTACCTCACTACTAAGGAGCACCTTCTCCTATATGGTTCCATCAAAGT	4560	4566
4501			
4501	CGTCTTGTT CAGTTACCTCACTACTAAGGAGCACCTTCTCCTATATGGTTCCATCAAAGT	4560	4566
	o o o o o o		
4561	TCCTCACTGGACTAAAAAGCAGCTCCACGAGGAAGTAAAAAGGACTTTAAAAGATACTGG	4620	4626
4561			
4561	TCCTCACTGGACTAAAAAGCAGCTCCACGAGGAAGTAAAAAGGACTTTAAAAGATACTGG	4620	4626
	o o o o o o		
4621	ACTATATAGCCATCGTCATAAGAGAGTTGGAACACTGTCAGGAGGCATGAAGAGGAAGTT	4680	4686
4621			
4621	ACTATATAGCCATCGTCATAAGAGAGTTGGAACACTGTCAGGAGGCATGAAGAGGAAGTT	4680	4686
	o o o o o o		
4681	ATCTATATCCATAGCTCTCATTTGGTGGATCAAGGGTAGTAATTTTGGATGAACCATCTAC	4740	4746
4681			
4681	ATCTATATCCATAGCTCTCATTTGGTGGATCAAGGGTAGTAATTTTGGATGAACCATCTAC	4740	4746
	o o o o o o		
4741	TGGAGTTGACCCATGTTCTCGCCGAAGTATATGGGATGTTATATCCAAGAACAAAAC TGC	4800	4806
4741			
4741	TGGAGTTGACCCATGTTCTCGCCGAAGTATATGGGATGTTATATCCAAGAACAAAAC TGC	4800	4806
	o o o o o o		
4801	CAGAACAATCATTCTGTCAACGCACCACTTGGACGAGGCTGAAGTGCTGAGTGACCGCAT	4860	4866
4801			
4801	CAGAACAATCATTCTGTCAACGCACCACTTGGACGAGGCTGAAGTGCTGAGTGACCGCAT	4860	4866
	o o o o o o		

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COMPARISON A: SEQ ID NO. 1 (top line) vs. SEQ ID NO. 2 (bottom line) (17 pages)

5941	GACAAAAGACCTTCGTTTTGATATAACAGGAGTCCCTGCCAATAGAACACTTGCCAAGGT	6000	6006
5704	GACAAAAGACCTTCGTTTTGATATAACAGGAGTCCCTGCCAATAGAACACTTGCCAAGGT	5763	5769
	o o o o o		
6001	ATGGTATGATCCAGAAGGCTATCACTCCCTTCCAGCTTACCTCAACAGCCTGAATAATTT	6060	6066
5764	ATGGTATGATCCAGAAGGCTATCACTCCCTTCCAGCTTACCTCAACAGCCTGAATAATTT	5823	5829
	o o o o o		
6061	CCTTCTGCGAGTTAACATGTCAAATACGATGCTGCCCGACATGGCATCATCATGTATAG	6120	6126
5824	CCTTCTGCGAGTTAACATGTCAAATACGATGCTGCCCGACATGGCATCATCATGTATAG	5883	5889
	o o o o o		
6121	CCATCCTTATCCAGGAGTGCAAGACCAAGAACAAGCCACAATCAGCAGTTTAATCGATAT	6180	6186
5884	CCATCCTTATCCAGGAGTGCAAGACCAAGAACAAGCCACAATCAGCAGTTTAATCGATAT	5943	5949
	o o o o o		
6181	TTTAGTGGCACTGTCTATCTTGATGGGCTACTCTGTCAACACCGCCAGCTTTGTACCTA	6240	6246
5944	TTTAGTGGCACTGTCTATCTTGATGGGCTACTCTGTCAACACCGCCAGCTTTGTACCTA	6003	6009
	o o o o o		
6241	TGTTGTAAGGGAACATCAAACCAAAGCCAAACAGTTGCAGCACATTTTCAGGCATTGGCGT	6300	6306
6004	TGTTGTAAGGGAACATCAAACCAAAGCCAAACAGTTGCAGCACATTTTCAGGCATTGGCGT	6063	6069
	o o o o o		
6301	GACATGCTACTGGGTAACAACTTCATTTATGACATGGTTTTCTACTTGGTGCCTGTAGC	6360	6366
6064	GACATGCTACTGGGTAACAACTTCATTTATGACATGGTTTTCTACTTGGTGCCTGTAGC	6123	6129
	o o o o o		
6361	GTTTTCAATTGGTATCATTGCGATTTTCAAATTACCTGCATTCTACAGTGAAAACAACCT	6420	6426
6124	GTTTTCAATTGGTATCATTGCGATTTTCAAATTACCTGCATTCTACAGTGAAAACAACCT	6183	6189
	o o o o o		
6421	AGGCGCTGTATCTCTCCTACTTCTCCTGTTTGGGCATGCAACATTTTCCTGGATGTACTT	6480	6486
6184	AGGCGCTGTATCTCTCCTACTTCTCCTGTTTGGGCATGCAACATTTTCCTGGATGTACTT	6243	6249
	o o o o o		

COMPARISON A: SEQ ID NO. 1 (top line) vs. SEQ ID NO. 2 (bottom line) (17 pages)

6481	GCTGGCTGGGCTCTTCCATGAAACAGGAATGGCCTTCATCACTTACGTCTGTGTCAACTT	6540	6546
6244	GCTGGCTGGGCTCTTCCATGAAACAGGAATGGCCTTCATCACTTACGTCTGTGTCAACTT	6303	6309
	o o o o o		
6541	GTTTTTTGGCATTAAATTCCATTGTTTCCCTGTCAGTGGTATACTTTCTTTCCAAGGAAAA	6600	6606
6304	GTTTTTTGGCATTAAATTCCATTGTTTCCCTGTCAGTGGTATACTTTCTTTCCAAGGAAAA	6363	6369
	o o o o o		
6601	GCCTAATGATCCGACTTTAGAACTTATTTCTGAAACCCTCAAGCGCATTTTCCTGATTTT	6660	6666
6364	GCCTAATGATCCGACTTTAGAACTTATTTCTGAAACCCTCAAGCGCATTTTCCTGATTTT	6423	6429
	o o o o o		
6661	CCCACAATTCTGTTTTGGCTACGGTTTGATTGAACTTTCTCAACAACAGTCGGTCCTAGA	6720	6726
6424	CCCACAATTCTGTTTTGGCTACGGTTTGATTGAACTTTCTCAACAACAGTCGGTCCTAGA	6483	6489
	o o o o o		
6721	CTTCTTAAAAGCATATGGAGTGGAATACCCAAATGAAACCTTTGAGATGAATAAACTAGG	6780	6786
6484	CTTCTTAAAAGCATATGGAGTGGAATACCCAAATGAAACCTTTGAGATGAATAAACTAGG	6543	6549
	o o o o o		
6781	TGCAATGTTTGTGGCTTTGGTTTCTCAGGGCACCATGTTTTTTTCCTTGCGACTCTTAAT	6840	6846
6544	TGCAATGTTTGTGGCTTTGGTTTCTCAGGGCACCATGTTTTTTTCCTTGCGACTCTTAAT	6603	6609
	o o o o o		
6841	CAACGAATCCCTGATAAAGAACTCAGGCTTTTCTTCAGAAAATTTAATTCTTCACATGT	6900	6906
6604	CAACGAATCCCTGATAAAGAACTCAGGCTTTTCTTCAGAAAATTTAATTCTTCACATGT	6663	6669
	o o o o o		
6901	AAGGGAGACAATAGATGAGGATGAAGATGTGCGGGCTGAGAGATTAAGAGTTGAGAGTGG	6960	6966
6664	AAGGGAGACAATAGATGAGGATGAAGATGTGCGGGCTGAGAGATTAAGAGTTGAGAGTGG	6723	6729
	o o o o o		
6961	TGCAGCTGAATTTGACTTGGTCCAACCTTTATTGTCTCACAAAGACCTACCAACTTATCCA	7020	7026
6724	TGCAGCTGAATTTGACTTGGTCCAACCTTTATTGTCTCACAAAGACCTACCAACTTATCCA	6783	6789
	o o o o o		

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COMPARISON A: SEQ ID NO. 1 (top line) vs. SEQ ID NO. 2 (bottom line) (17 pages)

7561	CAGCATGGAAGAATGTGAAGCTCTCTGTACCAGGTTGGCCATTATGGTGAATGGAAAGTT	7620	7626
7324	CAGCATGGAAGAATGTGAAGCTCTCTGTACCAGGTTGGCCATTATGGTGAATGGAAAGTT	7383	7389
	o o o o o		
7621	TCAATGTATTGGATCTTTGCAGCACATAAAGAGCAGGTTTGGACGAGGATTTACTGTCAA	7680	7686
7384	TCAATGTATTGGATCTTTGCAGCACATAAAGAGCAGGTTTGGACGAGGATTTACTGTCAA	7443	7449
	o o o o o		
7681	AGTTCACCTGAAGAATAACAAAGTGACCATGGAGACCCTCACAAAGTTCATGCAGCTGCA	7740	7746
7444	AGTTCACCTGAAGAATAACAAAGTGACCATGGAGACCCTCACAAAGTTCATGCAGCTGCA	7503	7509
	o o o o o		
7741	CTTTCACAAAACATACTTAAAAGATCAGCACCTCAGCATGCTAGAGTATCATGTACCAGT	7800	7806
7504	CTTTCACAAAACATACTTAAAAGATCAGCACCTCAGCATGCTAGAGTATCATGTACCAGT	7563	7569
	o o o o o		
7801	CACAGCAGGAGGAGTCGCAAACATTTTGTATCTGCTGGAAACCAACAAGACTGCTTTAAA	7860	7866
7564	CACAGCAGGAGGAGTCGCAAACATTTTGTATCTGCTGGAAACCAACAAGACTGCTTTAAA	7623	7629
	o o o o o		
7861	TATTACAAATTTCTTAGTGAGTCAGACCACTCTGGAAGAGGTTTTTCATCAACTTTGCCAA	7920	7926
7624	TATTACAAATTTCTTAGTGAGTCAGACCACTCTGGAAGAGGTTTTTCATCAACTTTGCCAA	7683	7689
	o o o o o		
7921	AGACCAGAAGTCCTATGAAACTGCTGATACCAGCAGCCAAGGTTCCACTATAAGTGTTGA	7980	7986
7684	AGACCAGAAGTCCTATGAAACTGCTGATACCAGCAGCCAAGGTTCCACTATAAGTGTTGA	7743	7749
	o o o o o		
7981	CTCACAAGATGACCAGATGGAGTCTTAACACTTCCAGCAAACCTCAATCTCAGCGTGTGAC	8040	8046
7744	CTCACAAGATGACCAGATGGAGTCTTAACACTTCCAGCAAACCTCAATCTCAGCGTGTGAC	7803	7809
	o o o o o		
8041	CAATGGCTTCATTTTGAAGAAAAGCCACAGAAGATACACTTCCGCAAGATATCTTCATTT	8100	8106
7804	CAATGGCTTCATTTTGAAGAAAAGCCACAGAAGATACACTTCCGCAAGATATCTTCATTT	7863	7869
	o o o o o		

COMPARISON A: SEQ ID NO. 1 (top line) vs. SEQ ID NO. 2 (bottom line) (17 pages)

8101	TAAAGTAAAGTAATATACTGTATGGAAAGTTACAAGTGTGTTAGACTAACAAGTAATTAT	8160	8166
7864	TAAAGTAAAGTAATATACTGTATGGAAAGTTACAAGTGTGTTAGACTAACAAGTAATTAT	7923	7929
	o o o o o		
8161	AAAAGGAAATTTTTCCTTCTAAGGTCAGTGAGTGTTGTTGCTACTGAAATGAATTCCTGT	8220	8226
7924	AAAAGGAAATTTTTCCTTCTAAGGTCAGTGAGTGTTGTTGCTACTGAAATGAATTCCTGT	7983	7989
	o o o o o		
8221	ATACTCAACACTGTGAGCATGCTAATGTATATGCTGGTGATTCTTATGCAAAGGTGAAGC	8280	8286
7984	ATACTCAACACTGTGAGCATGCTAATGTATATGCTGGTGATTCTTATGCAAAGGTGAAGC	8043	8049
	o o o o o		
8281	CACCTCAAGATGAATATCTTAATTTATTACTTTCAATAAAAAGACAGTTTAAAAGGCATG	8340	8346
8044	CACCTCAAGATGAATATCTTAATTTATTACTTTCAATAAAAAGACAGTTTAAAAGGCATG	8103	8109
	o o o o o		
8341	GATTTTGGTAGTTGAAATATAAGAGTGGAGAAGAAAAGTCAGATGGTTTGTGGCAGGTGC	8400	8406
8104	GATTTTGGTAGTTGAAATATAAGAGTGGAGAAGAAAAGTCAGATGGTTTGTGGCAGGTGC	8163	8169
	o o o o o		
8401	CACCGGGCAAGCAGACAACATAATTTATTTCCAGAAAACAACAGAATGAACATCATCATG	8460	8466
8164	CACCGGGCAAGCAGACAACATAATTTATTTCCAGAAAACAACAGAATGAACATCATCATG	8223	8229
	o o o o o		
8461	AATACATGAATCGGCTGTGATGTGTGAACTGCTAAGGGCCAAATGAACGTTTGNAGAGCA	8520	8526
8224	AATACATGAATCGGCTGTGATGTGTGAACTGCTAAGGGCCAAATGAACGTTTGNAGAGCA	8283	8289
	o o o o o		
8521	GTGGGCACAATGTTTACAATGTATGNGTATGTCACTTTCGGTACCNGTGAATGCATGGGG	8580	8586
8284	GTGGGCACAATGTTTACAATGTATGNGTATGTCACTTTCGGTACCNGTGAATGCATGGGG	8343	8349
	o o o o o		
8581	ACGTGCTGAACCCGAAAAAAAGTGCCTTTCCATAAGGACTGCAATAGAGAGGGCAATTTA	8640	8646
8344	ACGTGCTGAACCCGAAAAAAAGTGCCTTTCCATAAGGACTGCAATAGAGAGGGCAATTTA	8403	8409
	o o o o o		



COMPARISON B: SEQ ID NO. 5 (top line) vs. SEQ ID NO. 6 (bottom line) (15 pages)

1	METALASERLEUPHEHISGLNLEUGLNILELEUVALTRPLYSASNTRPLEUGLYVALLYS	60	66
1	METALASERLEUPHEHISGLNLEUGLNILELEUVALTRPLYSASNTRPLEUGLYVALLYS	60	66
61	ARGGLNPROLEUTRPTHRLEUVALLEUILELEUTRPPROVALILEILEPHEILEILELEU	120	126
61	ARGGLNPROLEUTRPTHRLEUVALLEUILELEUTRPPROVALILEILEPHEILEILELEU	120	126
121	ALAILETHRARGTHRLYSPHEPROPROTHRALALYSPROTHRCYSTYRLEUALAPROARG	180	186
121	ALAILETHRARGTHRLYSPHEPROPROTHRALALYSPROTHRCYSTYRLEUALAPROARG	180	186
181	ASNLEUPROSERTHRGLYPHEPHEPROPHELEUGLNTHRLEULEUCYSASPTHRA SPSE	240	246
181	ASNLEUPROSERTHRGLYPHEPHEPROPHELEUGLNTHRLEULEUCYSASPTHRA SPSE	240	246
241	LYSCYSLYASPTHPRPTYRGLYPROGLNASPLEULEUARGARGLYSGLYILEAS PASP	300	306
241	LYSCYSLYASPTHPRPTYRGLYPROGLNASPLEULEUARGARGLYSGLYILEAS PASP	300	306
301	ALALEUPHELYSASPSE RGLUILELEUARGLYSSERSE RASNLEUASPLYASPSERSE	360	366
301	ALALEUPHELYSASPSE RGLUILELEUARGLYSSERSE RASNLEUASPLYASPSERSE	360	366
361	LEUSERPHEGLNSERTHRGLNVALPROGLUARGARGHISALASERLEUALATHRVALPHE	420	426
361	LEUSERPHEGLNSERTHRGLNVALPROGLUARGARGHISALASERLEUALATHRVALPHE	420	426
421	PROSERPROSERSE RASPLEUGLUILEPROGLYTHRTYRTHRPHEASNGLYSERGLNVAL	480	486
421	PROSERPROSERSE RASPLEUGLUILEPROGLYTHRTYRTHRPHEASNGLYSERGLNVAL	480	486
481	LEUALAARGILELEUGLYLEUGLULYSLEULEULYSGLNASNSERTHRSE RGLUASPILE	540	546
481	LEUALAARGILELEUGLYLEUGLULYSLEULEULYSGLNASNSERTHRSE RGLUASPILE	540	546

COMPARISON B: SEQ ID NO. 5 (top line) vs. SEQ ID NO. 6 (bottom line) (15 pages)

[illegible]

COMPARISON B: SEQ ID NO. 5 (top line) vs. SEQ ID NO. 6 (bottom line) (15 pages)

1081	PHEGLUASPALALEULEUASNILESERALAASNSEPROTYRILEPROTYRLEUALACYS	1140	1146
1081	PHEGLUASPALALEULEUASNILESERALAASNSEPROTYRILEPROTYRLEUALACYS	1140	1146
1141	VALARGASNVALTHRASPSEERLEUALAARGGLYSERPROGLUASNLEUARGLEULEUGLN	1200	1206
1141	VALARGASNVALTHRASPSEERLEUALAARGGLYSERPROGLUASNLEUARGLEULEUGLN	1200	1206
1201	SERTHRILEARGPHELYSLYSSEERPHELEUARGASNGLYSERTYRGLUASPTYRPHEPRO	1260	1266
1201	SERTHRILEARGPHELYSLYSSEERPHELEUARGASNGLYSERTYRGLUASPTYRPHEPRO	1260	1266
1261	PROVALPROGLUVALLEULYSSEERLYSLEUSERGLNLEUARGASNLEUTHRGLULEULEU	1320	1326
1261	PROVALPROGLUVALLEULYSSEERLYSLEUSERGLNLEUARGASNLEUTHRGLULEULEU	1320	1326
1321	CYSGLUSERGLUTHRPHESERLEUILEGLULYSSEERCYSGLNLEUSERASPMETSERPHE	1380	1386
1321	CYSGLUSERGLUTHRPHESERLEUILEGLULYSSEERCYSGLNLEUSERASPMETSERPHE	1380	1386
1381	GLYSERLEUCYSGLUGLUSERGLUPHEASPLEUGLNLEULEUGLUALAALAGLULEUGLY	1440	1446
1381	GLYSERLEUCYSGLUGLUSERGLUPHEASPLEUGLNLEULEUGLUALAALAGLULEUGLY	1440	1446
1441	THRGLUILEALAALASERLEULEUTYRHSASPASNVALILESERLYSLYSVALARGASP	1500	1506
1441	THRGLUILEALAALASERLEULEUTYRHSASPASNVALILESERLYSLYSVALARGASP	1500	1506
1501	LEULEUTHRGLYASPPROSERLYSILEASNLEUASNMETASPGNLPHELEUGLUGLNALA	1560	1566
1501	LEULEUTHRGLYASPPROSERLYSILEASNLEUASNMETASPGNLPHELEUGLUGLNALA	1560	1566
1561	LEUGLNMETASNTYRLEUGLUASNILETHRGLNLEUILEPROILEILEGLUALAMETLEU	1620	1626
1561	LEUGLNMETASNTYRLEUGLUASNILETHRGLNLEUILEPROILEILEGLUALAMETLEU	1620	1626

COMPARISON B: SEQ ID NO. 5 (top line) vs. SEQ ID NO. 6 (bottom line) (15 pages)

1621	HISVALASNASN SERALAAS PALASERGLULYSPROGLYGLNLEULEUGLUMETPHELYS	1680	1686
1621	HISVALASNASN SERALAAS PALASERGLULYSPROGLYGLNLEULEUGLUMETPHELYS	1680	1686
1681	ASNVALGLUGLULEULYSGLUASPLEUARGARGTHRTHRGLYMETSERASNARGTHRILE	1740	1746
1681	ASNVALGLUGLULEULYSGLUASPLEUARGARGTHRTHRGLYMETSERASNARGTHRILE	1740	1746
1741	ASPLYSLEULEUALAILEPROILEPROASPASNARGALAGLUILEILESERGLNVALPHE	1800	1806
1741	ASPLYSLEULEUALAILEPROILEPROASPASNARGALAGLUILEILESERGLNVALPHE	1800	1806
1801	TRPLEUHISSERCYSASPTHRASNIETHRTHRPROLYSLEUGLUASPALAMETLYSGLU	1860	1866
1801	TRPLEUHISSERCYSASPTHRASNIETHRTHRPROLYSLEUGLUASPALAMETLYSGLU	1860	1866
1861	PHECYSASNLEUSERLEUSERGLUARGSERARGGLNSERTYRLEUILEGLYLEUTHRLEU	1920	1926
1861	PHECYSASNLEUSERLEUSERGLUARGSERARGGLNSERTYRLEUILEGLYLEUTHRLEU	1920	1926
1921	LEUHISTYRLEUASNILETYRASNPHETHRASP LYSVALPHEPHEPROARGLYSASPGLN	1980	1986
1921	LEUHISTYRLEUASNILETYRASNPHETHRASP LYSVALPHEPHEPROARGLYSASPGLN	1980	1986
1981	LYSPROVALGLULYSMETMETGLULEUPHEILEARGLEULYSGLUILELEUASNGLNMET	2040	2046
1981	LYSPROVALGLULYSMETMETGLULEUPHEILEARGLEULYSGLUILELEUASNGLNMET	2040	2046
2041	ALASERGLYTHRHRISPROLEULEUASPLYSMETARGSERLEULYSGLNMETHISLEUPRO	2100	2106
2041	ALASERGLYTHRHRISPROLEULEUASPLYSMETARGSERLEULYSGLNMETHISLEUPRO	2100	2106
2101	ARGSERVALPROLEUTHRGLNALAMETTYRARGSERASNARGMETASNTHRPROGLNGLY	2160	2166
2101	ARGSERVALPROLEUTHRGLNALAMETTYRARGSERASNARGMETASNTHRPROGLNGLY	2160	2166

COMPARISON B: SEO ID NO. 5 (top line) vs. SEQ ID NO. 6 (bottom line) (15 pages)

2161	SERPHERSERTHRILESERGLNALALEUCYSSERGLNGLYILETHRTHRGLUTYRLEUTHR	2220	2226
2161	SERPHERSERTHRILESERGLNALALEUCYSSERGLNGLYILETHRTHRGLUTYRLEUTHR	2220	2226
2221	ALAMETLEUPROSERSERGLNARGPROLYSGLYASNHISTRHLYSASPPHELEUTHRTRYR	2280	2286
2221	ALAMETLEUPROSERSERGLNARGPROLYSGLYASNHISTRHLYSASPPHELEUTHRTRYR	2280	2286
2281	LYSLEUTHRLYSGLUGLNILEALASERLYSTYRGLYILEPROILEASNTHRTHRPROPHE	2340	2346
2281	LYSLEUTHRLYSGLUGLNILEALASERLYSTYRGLYILEPROILEASNTHRTHRPROPHE	2340	2346
2341	CYSPHERSERLEUTYRLYSASPILEILEASNMETPROALAGLYPROVALILETRPALAPHE	2400	2406
2341	CYSPHERSERLEUTYRLYSASPILEILEASNMETPROALAGLYPROVALILETRPALAPHE	2400	2406
2401	LEULYSPROMETLEULEUGLYARGILELEUHISSALAPROTYRASNPVALTHRLYSALA	2460	2466
2401	LEULYSPROMETLEULEUGLYARGILELEUHISSALAPROTYRASNPVALTHRLYSALA	2460	2466
2461	ILEMETGLULYSSERASNVALTHRLEUARGGLNLEUALAGLULEUARGGLULYSSERGLN	2520	2526
2461	ILEMETGLULYSSERASNVALTHRLEUARGGLNLEUALAGLULEUARGGLULYSSERGLN	2520	2526
2521	GLUTRPMETASPLYSSERPROLEUPHEMETASNSERPHEHISLEULEUASNGLNALAILE	2580	2586
2521	GLUTRPMETASPLYSSERPROLEUPHEMETASNSERPHEHISLEULEUASNGLNALAILE	2580	2586
2581	PROMETLEUGLNASNTHRLEUARGASNPROPHEVALGLNVALPHEVALLYSPHERSERVAL	2640	2646
2581	PROMETLEUGLNASNTHRLEUARGASNPROPHEVALGLNVALPHEVALLYSPHERSERVAL	2640	2646
2641	GLYLEUASPALAVALGLULEULEULYSGLNILEASPGULEUASPILELEUARGLEULYS	2700	2706
2641	GLYLEUASPALAVALGLULEULEULYSGLNILEASPGULEUASPILELEUARGLEULYS	2700	2706

COMPARISON B: SEQ ID NO. 5 (top line) vs. SEQ ID NO. 6 (bottom line) (15 pages)

2701	LEUGLUASNASNILEASPILEILEASPGLNLEUASNTHRLEUSERSERLEUTHRVALASN	2760	2766
2701	LEUGLUASNASNILEASPILEILEASPGLNLEUASNTHRLEUSERSERLEUTHRVALASN	2760	2766
2761	ILESERSERCYSVALLEUTYRASPARGILEGLNALAALALYSTHRILEASPGLUMETGLU	2820	2826
2761	ILESERSERCYSVALLEUTYRASPARGILEGLNALAALALYSTHRILEASPGLUMETGLU	2820	2826
2821	ARGGLUALALYSARGLEUTYRLYSSERASNGLULEUPHEGLYSERVALILEPHELYSLEU	2880	2886
2821	ARGGLUALALYSARGLEUTYRLYSSERASNGLULEUPHEGLYSERVALILEPHELYSLEU	2880	2886
2881	PROSERASNARGSERTRPHISARGGLYTYRASPSERGLYASNVALPHELEUPROPROVAL	2940	2946
2881	PROSERASNARGSERTRPHISARGGLYTYRASPSERGLYASNVALPHELEUPROPROVAL	2940	2946
2941	ILELYSTYRTHRILEARGMETSERLEULYSTHRALAGLNTHRTHRARGSERLEUARGTHR	3000	3006
2941	ILELYSTYRTHRILEARGMETSERLEULYSTHRALAGLNTHRTHRARGSERLEUARGTHR	3000	3006
3001	LYSILETRPALAPROGLYPROHISASNSENPROSERHISASNGLNILETYRGLYARGALA	3060	3066
3001	LYSILETRPALAPROGLYPROHISASNSENPROSERHISASNGLNILETYRGLYARGALA	3060	3066
3061	PHEILETYRLEUGLNASPSEIRILEGLUARGALAILEILEGLULEUGLNTHRGLYARGASN	3120	3126
3061	PHEILETYRLEUGLNASPSEIRILEGLUARGALAILEILEGLULEUGLNTHRGLYARGASN	3120	3126
3121	SERGLNGLUILEALAVAGLNVALGLNALAILEPROTYRPROCYSPHEMETLYSASPASN	3180	3186
3121	SERGLNGLUILEALAVAGLNVALGLNALAILEPROTYRPROCYSPHEMETLYSASPASN	3180	3186
3181	PHELEUTHRSERVALSERTYRSEIRLEUPROILEVALLEUMETVALALATRPVALVALPHE	3240	3246
3181	PHELEUTHRSERVALSERTYRSEIRLEUPROILEVALLEUMETVALALATRPVALVALPHE	3240	3246

COMPARISON B: SEQ ID NO. 5 (top line) vs. SEQ ID NO. 6 (bottom line) (15 pages)

3781	SERPHEILETYRPHELEUILEALATRPTYRVALARGASNVALPHEPROGLYTHRTRYRGly	3840	3846
3781	SERPHEILETYRPHELEUILEALATRPTYRVALARGASNVALPHEPROGLYTHRTRYRGly	3840	3846
3841	METALAALAPROTRPTYRPHEPROILELEUPROSEPTYRTRPLYSGLUARGPHEGLYCYS	3900	3906
3841	METALAALAPROTRPTYRPHEPROILELEUPROSEPTYRTRPLYSGLUARGPHEGLYCYS	3900	3906
3901	ALAGLUVALLYSPROGLULYSSERASNGLYLEUMETPHETHRASNILEMETMETGLNASN	3960	3966
3901	ALAGLUVALLYSPROGLULYSSERASNGLYLEUMETPHETHRASNILEMETMETGLNASN	3960	3966
3961	THRASNPROSERALASERPROGLUTYRMETPHESERSERASNILEGLUPROGLUPROLYS	4020	4026
3961	THRASNPROSERALASERPROGLUTYRMETPHESERSERASNILEGLUPROGLUPROLYS	4020	4026
4021	ASPLEUTHRVALGLYVALALALEUHSGLYVALTHRLYSILETYRGLYSERLYSVALALA	4080	4086
4021	ASPLEUTHRVALGLYVALALALEUHSGLYVALTHRLYSILETYRGLYSERLYSVALALA	4080	4086
4081	VALASPASNLEUASNLEUASNPHETYRGLUGLYHISILETHRSEERLEULEUGLYPROASN	4140	4146
4081	VALASPASNLEUASNLEUASNPHETYRGLUGLYHISILETHRSEERLEULEUGLYPROASN	4140	4146
4141	GLYALAGLYLYSTHRTTHRTHRILESERMETLEUTHRGLYLEUPHEGLYALASERALAGLY	4200	4206
4141	GLYALAGLYLYSTHRTTHRTHRILESERMETLEUTHRGLYLEUPHEGLYALASERALAGLY	4200	4206
4201	THRIEPHEVALTYRGLYLYSASPILELYSTHRASPLEUHSITHRVALARGLYSASNMET	4260	4266
4201	THRIEPHEVALTYRGLYLYSASPILELYSTHRASPLEUHSITHRVALARGLYSASNMET	4260	4266
4261	GLYVALCYSMETGLNHSASPVALLEUPHESERTYRLEUTHRTHRLYSGLUHSLEULEU	4320	4326
4261	GLYVALCYSMETGLNHSASPVALLEUPHESERTYRLEUTHRTHRLYSGLUHSLEULEU	4320	4326

COMPARISON B: SEQ ID NO. 5 (top line) vs. SEQ ID NO. 6 (bottom line) (15 pages)

4321	LEUTYRGLYSERILELYSVALPROHISTRPTHRLYSLSYGLNLEUHSGLUGLUVALLYS	4380	4386
4321	LEUTYRGLYSERILELYSVALPROHISTRPTHRLYSLSYGLNLEUHSGLUGLUVALLYS	4380	4386
4381	ARGTHRLEULYSASPTHRLYLEUTYRSEHISARGHISLSYARGVALGLYTHRLEUSER	4440	4446
4381	ARGTHRLEULYSASPTHRLYLEUTYRSEHISARGHISLSYARGVALGLYTHRLEUSER	4440	4446
4441	GLYGLYMETLYSARGLYSLEUSERILESERILEALALEUILEGLYGLYSERARGVALVAL	4500	4506
4441	GLYGLYMETLYSARGLYSLEUSERILESERILEALALEUILEGLYGLYSERARGVALVAL	4500	4506
4501	ILELEUASPGULUPROSERTHRGLYVALASPPROCYSSERARGARGSERILETRPASPVAL	4560	4566
4501	ILELEUASPGULUPROSERTHRGLYVALASPPROCYSSERARGARGSERILETRPASPVAL	4560	4566
4561	ILESERLYSASNLYSTHRLAARGTHRIEILELEUSERTHRHISHISLEUASPGLUALA	4620	4626
4561	ILESERLYSASNLYSTHRLAARGTHRIEILELEUSERTHRHISHISLEUASPGLUALA	4620	4626
4621	GLUVALLEUSERASPARGILEALAPHELEUGLUGLNGLYGLYLEUARGCYSCYSGLYSER	4680	4686
4621	GLUVALLEUSERASPARGILEALAPHELEUGLUGLNGLYGLYLEUARGCYSCYSGLYSER	4680	4686
4681	PROPHETRYLEULYSGLUALAPHEGLYASPGLYTYRHISLEUTHRLEUTHRLYSLSYLS	4740	4746
4681	PROPHETRYLEULYSGLUALAPHEGLYASPGLYTYRHISLEUTHRLEUTHRLYSLSYLS	4740	4746
4741	SERPROASNLEUASNALAAASNALAVALCYSASPTHMETALAVALTHRALAMETILEGLN	4800	4806
4741	-----	4740	4746
4801	SERHISLEUPROGLUALATYRLEULYSGLUASPILEGLYGLYLULEUVALTYRVALLEU	4860	4866
4741	-----	4740	4746

COMPARISON B: SEQ ID NO. 5 (top line) vs. SEQ ID NO. 6 (bottom line) (15 pages)

4861	PROPHESERTHRLYSVALSERGLYALATYRLEUSERLEULEUARGALALEUASPASN	4920	4926
4741	-----	4740	4746
4921	GLYMETGLYASPLEUASNILEGLYCYSTYRGLYILESERASPTHRTHRVALGLUGLUVAL	4980	4986
4741	-----VAL	4743	4749
4981	PHELEUASNLEUTHRLYSGLUSERGLNLYSASNSEALAMETSERLEUGLUHISLEUTHR	5040	5046
4744	PHELEUASNLEUTHRLYSGLUSERGLNLYSASNSEALAMETSERLEUGLUHISLEUTHR	4803	4809
5041	GLNLYSLYSILEGLYASNSEALASNGLYILESERTHRPROASPASPLEUSERVAL	5100	5106
4804	GLNLYSLYSILEGLYASNSEALASNGLYILESERTHRPROASPASPLEUSERVAL	4863	4869
5101	SERSERSERASNPHETHRASPARGASPPLYSILELEUTHRARGGLYGLUARGLEUASP	5160	5166
4864	SERSERSERASNPHETHRASPARGASPPLYSILELEUTHRARGGLYGLUARGLEUASP	4923	4929
5161	GLYPHEGLYLEULEULEULYSLSILEMETALAILELEULELYSARGPHEHISHISXAA	5220	5226
4924	GLYPHEGLYLEULEULEULYSLSILEMETALAILELEULELYSARGPHEHISHISALA	4983	4989
5221	ARGARGASNTRPLYSGLYLEULEALAGLNVALILELEUPROILEVALPHEVALTHRTHR	5280	5286
4984	ARGARGASNTRPLYSGLYLEULEALAGLNVALILELEUPROILEVALPHEVALTHRTHR	5043	5049
5281	ALAMETGLYLEUGLYTHRLEUARGASNSEALASNSERTYRPROGLUILEGLNILESER	5340	5346
5044	ALAMETGLYLEUGLYTHRLEUARGASNSEALASNSERTYRPROGLUILEGLNILESER	5103	5109
5341	PROSERLEUTYRGLYTHRSEALUGLNTHRALAPHETYRALAASNTRYRHISPROSERTHR	5400	5406
5104	PROSERLEUTYRGLYTHRSEALXAGLNTHRALAPHETYRALAASNTRYRHISPROSERTHR	5163	5169

COMPARISON B: SEQ ID NO. 5 (top line) vs. SEQ ID NO. 6 (bottom line) (15 pages)

5401	GLUALALEUVALSERALAMETTRPASPPHEPROGLYILEASPASNMETCYSLEUASNTHR	5460	5466
5164	GLUALALEUVALSERALAMETTRPASPPHEPROGLYILEASPASNMETCYSLEUASNTHR	5223	5229
5461	SERASPLEUGLNCYSLEUASNLYSASPSEERLEUGLULYSTRPASNTHRSEERGLYGLUPRO	5520	5526
5224	SERASPLEUGLNCYSLEUASNLYSASPSEERLEUGLULYSTRPASNTHRSEERGLYGLUPRO	5283	5289
5521	ILETHRASNPHGLYVALCYSSERCYSSERGLUASNVALGLNGLUCYSPROLYSPHEASN	5580	5586
5284	ILETHRASNPHGLYVALCYSSERCYSSERGLUASNVALGLNGLUCYSPROLYSPHEASN	5343	5349
5581	TYRSEERPROPHISARGARGTHRSEERSEERGLNVALILETYRASNLEUTHRGLYGLN	5640	5646
5344	TYRSEERPROPHISARGARGTHRSEERSEERGLNVALILETYRASNLEUTHRGLYGLN	5403	5409
5641	ARGVALGLUASNSEERLEUILESEERTHRALAASNGLUPHEVALGLNLYSARGTYRGLYGLY	5700	5706
5404	ARGVALGLUASNSEERLEUILESEERTHRALAASNGLUPHEVALGLNLYSARGTYRGLYGLY	5463	5469
5701	TRPSEERPHGLYLEUPROLEUTHRLYSASPLEUARGPHEASPILETHRGLYVALPROALA	5760	5766
5464	TRPSEERPHGLYLEUPROLEUTHRLYSASPLEUARGPHEASPILETHRGLYVALPROALA	5523	5529
5761	ASNARGTHRLEUALALYSVALTRPTYRASPPROGLUGLYTYRHISSEERLEUPROALATYR	5820	5826
5524	ASNARGTHRLEUALALYSVALTRPTYRASPPROGLUGLYTYRHISSEERLEUPROALATYR	5583	5589
5821	LEUASNSEERLEUASNASNPHLEULEUARGVALASNMETSEERLYSTYRASPALAALAARG	5880	5886
5584	LEUASNSEERLEUASNASNPHLEULEUARGVALASNMETSEERLYSTYRASPALAALAARG	5643	5649
5881	HISGLYILEILEMETTYRSEERHISPROTYRPROGLYVALGLNASPGLNGLUGLNALATHR	5940	5946
5644	HISGLYILEILEMETTYRSEERHISPROTYRPROGLYVALGLNASPGLNGLUGLNALATHR	5703	5709

COMPARISON B: SEO ID NO. 5 (top line) vs. SEO ID NO. 6 (bottom line) (15 pages)

5941	ILESERSERLEUILEASPILELEUVALALALEUSERILELEUMETGLYTYRSERVALTHR	6000	6006
5704	ILESERSERLEUILEASPILELEUVALALALEUSERILELEUMETGLYTYRSERVALTHR	5763	5769
	o o o o o		
		
6001	THRALASERPHEVALTHRTRYRVALVALARGGLUHIISGLNTHRLYSALALYSGLNLEUGLN	6060	6066
5764	THRALASERPHEVALTHRTRYRVALVALARGGLUHIISGLNTHRLYSALALYSGLNLEUGLN	5823	5829
	o o o o o		
		
6061	HISILESERGLYILEGLYVALTHRCYSTYRTRPVALTHRASNPHEILETYRASPMETVAL	6120	6126
5824	HISILESERGLYILEGLYVALTHRCYSTYRTRPVALTHRASNPHEILETYRASPMETVAL	5883	5889
	o o o o o		
		
6121	PHETYRLEUVALPROVALALAPHESERILEGLYILEILEALAILEPHELYSLEUPROALA	6180	6186
5884	PHETYRLEUVALPROVALALAPHESERILEGLYILEILEALAILEPHELYSLEUPROALA	5943	5949
	o o o o o		
		
6181	PHETYRSEGLUASNASNLEUGLYALAVALSERLEULEULEULEULEUPHEGLYHISALA	6240	6246
5944	PHETYRSEGLUASNASNLEUGLYALAVALSERLEULEULEULEULEUPHEGLYHISALA	6003	6009
	o o o o o		
		
6241	THRPHESETRPMETTYRLEULEUALAGLYLEUPHEHISGLUTHRGLYMETALAPHEILE	6300	6306
6004	THRPHESETRPMETTYRLEULEUALAGLYLEUPHEHISGLUTHRGLYMETALAPHEILE	6063	6069
	o o o o o		
		
6301	THRTRYRVALCYSVASASNLEUPHEPHEGLYILEASNSEIRILEVALSERLEUSERVALVAL	6360	6366
6064	THRTRYRVALCYSVASASNLEUPHEPHEGLYILEASNSEIRILEVALSERLEUSERVALVAL	6123	6129
	o o o o o		
		
6361	TYRPHELEUSERLYSGLULYSPROASNAPPROTHRLEUGLULEUILESERGLUTHRLEU	6420	6426
6124	TYRPHELEUSERLYSGLULYSPROASNAPPROTHRLEUGLULEUILESERGLUTHRLEU	6183	6189
	o o o o o		
		
6421	LYSARGILEPHELEUILEPHEPROGLNPHECYSPEGLYTYRGLYLEUILEGLLULEUSER	6480	6486
6184	LYSARGILEPHELEUILEPHEPROGLNPHECYSPEGLYTYRGLYLEUILEGLLULEUSER	6243	6249
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14

COMPARISON B: SEQ ID NO. 5 (top line) vs. SEQ ID NO. 6 (bottom line) (15 pages)

7561	LEUGLUTYRHISVALPROVALTHRAGLYGLYVALALAASNILEPHEASPLEULEUGLU	7620	7626
7324	LEUGLUTYRHISVALPROVALTHRAGLYGLYVALALAASNILEPHEASPLEULEUGLU	7383	7389
	o o o o o o		
7621	THRASNLYSTHRALALEUASNILETHRASNPHELEUVALSERGLNTHRTHRLEUGLUGLU	7680	7686
7384	THRASNLYSTHRALALEUASNILETHRASNPHELEUVALSERGLNTHRTHRLEUGLUGLU	7443	7449
	o o o o o o		
7681	VALPHEILEASNPEALALYSASPGLNLYSSERTYRGLUTHRALAASPTHRSESRERGLN	7740	7746
7444	VALPHEILEASNPEALALYSASPGLNLYSSERTYRGLUTHRALAASPTHRSESRERGLN	7503	7509
	o o o o o o		
7741	GLYSERTHRILESERVALASPSEGLNASPASPGLNMETGLUSER	7785	7791
7504	GLYSERTHRILESERVALASPSEGLNASPASPGLNMETGLUSER	7548	7554
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